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14/34

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Filed on 18 May 2000 (18.05.2000)

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(75) Inventors/Applicants (for US only): **NEVILLE, David**,

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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Published:

— with international search report

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21 March 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **IMMUNOTOXIN FUSION PROTEINS AND MEANS FOR EXPRESSION THEREOF**

(57) Abstract: The present invention described and shown in the specification and drawings provides novel recombinant DT-based immunotoxins, and, more specifically anti-T cell immunotoxin fusion proteins. Also provided are immunotoxins that can be expressed in bacterial, yeast, or mammalian cells. The invention also provides means for expression of the immunotoxin fusion protein. It is emphasized that this abstract is provided to comply with the rules requiring an abstract that will allow a searcher or other reader to quickly ascertain the subject matter of the technical disclosure. It is submitted with the understanding that it will not be used to interpret or limit the scope or meaning of the claims.

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## INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 01/16125

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/62 C07K19/00 C12N15/63 C12N1/19 C12N1/21  
 C12N5/10 //C07K16/28, C07K14/34

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EMBASE, CHEM ABS Data, WPI Data, PAJ, EPO-Internal, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 39363 A (THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES ET AL.) 11 September 1998 (1998-09-11)	1, 15-26, 29, 30, 33-41, 45, 54-67, 79, 80, 92-97, 116-119
Y	examples 8-10 claims figures 11, 14	31, 32, 43, 44, 77, 78, 99-103
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Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

## \* Special categories of cited documents:

- \*A\* document defining the general state of the art which is not considered to be of particular relevance
- \*E\* earlier document but published on or after the international filing date
- \*L\* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- \*O\* document referring to an oral disclosure, use, exhibition or other means
- \*P\* document published prior to the international filing date but later than the priority date claimed

\*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

\*Y\* document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

\*G\* document member of the same patent family

Date of the actual completion of the international search

26 November 2001

Date of mailing of the international search report

10/12/2001

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/16125

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 98 39425 A (THE SECRETARY, THE DEPARTMENT OF HEALTH AND HUMAN SERVICES) 11 September 1998 (1998-09-11)  the whole document	31,32, 43,44, 77,78, 99-103
X	WO 96 32137 A (THE SECRETARY, THE DEPARTMENT OF HEALTH AND HUMAN SERVICES ET AL.) 17 October 1996 (1996-10-17)  examples 9-11 claims 1,22,23	1,15-26, 29,30, 33-41, 45, 54-67, 79,80, 92-97, 116-119
X	J. THOMPSON ET AL.: "An anti-CD3 single-chain immunotoxin with a truncated diphtheria toxin avoids inhibition by pre-existing antibodies in human blood." THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 47, 24 November 1995 (1995-11-24), pages 28037-28041, XP002083389 Baltimore, MD, USA the whole document	1,15-26, 33-40, 116-119
Y		29,30, 41, 43-45, 54-67, 79,80, 92-97, 101,102
Y	S. MA ET AL.: "Expression and characterization of a divalent chimeric anti-human CD3 single-chain antibody." SCANDINAVIAN JOURNAL OF IMMUNOLOGY, vol. 43, no. 2, February 1996 (1996-02), pages 134-139, XP002083387 Oxford, GB the whole document	29,30, 41,45, 54-67, 79,80, 92-97
Y	M. KIEKE ET AL.: "Isolation of anti-T cell receptor scFv mutants by yeast surface display." PROTEIN ENGINEERING, vol. 10, no. 11, 1997, pages 1303-1310, XP002064403 Oxford, GB abstract	43,44, 101,102

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## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/16125

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	D. VALLERA ET AL.: "Anti-graft-versus-host disease effect of DT390-anti-CD3sFv, a single-chain Fv fusion immunotoxin specifically targeting the CD3-epsilon moiety of the T-cell receptor." BLOOD, vol. 88, no. 6, 15 September 1996 (1996-09-15), pages 2342-2353, XP000645998 Philadelphia, PA, USA the whole document  -----	1,15-26, 33-40, 116-119
A	S. MA ET AL.: "Genetic construction and characterization of an anti-monkey CD3 single-chain immunotoxin with a truncated diphtheria toxin." BIOCONJUGATE CHEMISTRY, vol. 8, no. 5, September 1997 (1997-09), pages 695-701, XP002183986 Washington, DC, USA abstract  -----	1,15-26, 33-40, 116-119

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/16125

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9839363	A	11-09-1998	AU 733898 B2	31-05-2001
			AU 6542698 A	22-09-1998
			EP 1015496 A2	05-07-2000
			WO 9839363 A2	11-09-1998
WO 9839425	A	11-09-1998	AU 736501 B2	26-07-2001
			AU 6445998 A	22-09-1998
			EP 0968282 A2	05-01-2000
			WO 9839425 A2	11-09-1998
WO 9632137	A	17-10-1996	AU 5663796 A	30-10-1996
			CA 2218166 A1	17-10-1996
			EP 0830146 A2	25-03-1998
			WO 9632137 A2	17-10-1996
			US 5762927 A	09-06-1998

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<210> 23

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

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1 5

<210> 24

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 24

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21

<210> 25

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 25

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1 5 10 15  
Gly Ala Asp Ala Ala  
20

<210> 26

<211> 895

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 26

Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu  
1 5 10 15

Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile  
20 25 30  
Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp  
35 40 45  
Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala  
50 55 60

Gly 65	Tyr	Ser	Val	Asp	Asn 70	Glu	Asn	Pro	Leu	Ser 75	Gly	Lys	Ala	Gly	Gly 80
Val	Val	Lys	Val	Thr 85	Tyr	Pro	Gly	Leu	Thr 90	Lys	Val	Leu	Ala	Leu	Lys 95
Val	Asp	Asn	Ala	Glu	Thr	Ile	Lys	Lys 100	Glu	Leu	Gly	Leu	Ser	Leu	Thr 110
Glu	Pro	Leu	Met	Glu	Gln	Val	Gly	Thr 105	Glu	Glu	Phe	Ile	Lys	Arg	Phe 115
Gly	Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe	Ala	Glu	Gly 120
Ser 125	Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu	Gln	Ala	Lys	Ala	Leu 130
Ser 135	Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu	Thr	Arg	Gly	Lys	Arg	Gly	Gln 140
Asp	Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly	Asn	Arg	Val 145
Arg	Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp	Trp	Asp 150
Val	Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys	Glu	His 155
Gly	Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Ala	Lys	Thr	Val	Ser 160
Glu	Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln	Thr	Ala	Leu 165
Glu	His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly	Thr	Asn	Pro 170
Val	Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn	Val	Ala	Gln 175
Val	Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Thr	Ala	Ala 180
Leu	Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala	Asp	Gly 185
Ala	Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile	Ala	Leu 190
Ser	Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu	Leu	Val 195
Asp	Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile	Ile	Asn	Leu 200
Phe	Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr	Ser	Pro	Gly 205
His	Lys	Thr	Gln	Pro	Phe	Leu	Pro	Trp	Asp	Ile	Gln	Met	Thr	Gln	Thr 210
Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys 215
Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys 220
Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His 225
Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr 230
Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe 235
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly	Gly	Thr	Lys 240
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly 245
Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys 250
Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe 255

19

Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu  
 545 550 555 560  
 Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn  
 565 570 575  
 Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
 580 585 590  
 Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val  
 595 600 605  
 Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe  
 610 615 620  
 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
 625 630 635 640  
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met  
 645 650 655  
 Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr  
 660 665 670  
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr  
 675 680 685  
 Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser  
 690 695 700  
 Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly  
 705 710 715 720  
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala  
 725 730 735  
 Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly  
 740 745 750  
 Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 755 760 765  
 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
 770 775 780  
 Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly  
 785 790 795 800  
 Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly  
 805 810 815  
 Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser  
 820 825 830  
 Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys  
 835 840 845  
 Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp  
 850 855 860  
  
 Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp  
 865 870 875 880  
 Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe Ser  
 885 890 896

&lt;210&gt; 27

&lt;211&gt; 895

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

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 20 25 30



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 35 40 45  
 Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala Gly  
 50 55 60  
 Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly Val  
 65 70 75 80  
 Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val  
 85 90 95  
 Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu  
 100 105 110  
 Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe Gly  
 115 120 125  
 Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly Ser  
 130 135 140  
 Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu Ser  
 145 150 155 160  
 Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln Asp  
 165 170 175  
 Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val Arg  
 180 185 190  
 Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val  
 195 200 205  
 Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly  
 210 215 220  
 Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser Glu  
 225 230 235 240  
 Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu  
 245 250 255  
 His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val  
 260 265 270  
 Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val  
 275 280 285  
 Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu  
 290 295 300  
  
 Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala  
 305 310 315 320  
 Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser  
 325 330 335  
 Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp  
 340 345 350  
 Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe  
 355 360 365  
 Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His  
 370 375 380  
 Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr Thr  
 385 390 395 400  
 Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg  
 405 410 415  
 Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro  
 420 425 430  
 Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser  
 435 440 445  
 Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser  
 450 455 460  
 Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys  
 465 470 475 480  
 Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr Lys Leu  
 485 490 495  
 Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 500 505 510

Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro  
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 Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu  
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 Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln  
                                   565                  570                  575  
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                                   580                  585                  590  
 Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
                                   595                  600                  605  
 Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp  
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 625                                  630                  635                  640  
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                                   645                  650                  655  
 Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile  
                                   660                  665                  670  
 Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln  
                                   675                  680                  685  
 Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg  
                                   690                  695                  700  
 Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr  
 705                                  710                  715                  720  
 Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr  
                                   725                  730                  735  
  
 Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly  
                                   740                  745                  750  
 Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser  
                                   755                  760                  765  
 Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu  
                                   770                  775                  780  
 Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr  
 785                                  790                  795                  800  
 Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys  
                                   805                  810                  815  
 Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr  
                                   820                  825                  830  
 Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser  
                                   835                  840                  845  
 Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser  
                                   850                  855                  860  
 Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp  
 865                                  870                  875                  880  
 Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe Ser  
                                   885                  890                  895

&lt;210&gt; 28

&lt;211&gt; 899

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 28

Tyr Val Glu Phe Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe  
 1                                  5                  10                  15



23

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 500 505 510  
 Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
 515 520 525  
 Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly  
 530 535 540  
 Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly  
 545 550 555 560  
 Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser  
 565 570 575  
 Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys  
 580 585 590

Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp  
 595 600 605  
 Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp  
 610 615 620  
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser  
 625 630 635 640  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp  
 645 650 655  
 Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp  
 660 665 670  
 Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu  
 675 680 685  
 Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr  
 690 695 700  
 Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser  
 705 710 715 720  
 Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu  
 725 730 735  
 Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr  
 740 745 750  
 Phe Ala Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly  
 755 760 765  
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser  
 770 775 780  
 Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys  
 785 790 795 800  
 Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln  
 805 810 815  
 Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys  
 820 825 830  
 Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr  
 835 840 845  
 Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr  
 850 855 860  
 Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly  
 865 870 875 880  
 Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr  
 885 890 895  
 Val Phe Ser

&lt;210&gt; 29

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:/Note =

## synthetic construct

&lt;400&gt; 29

```

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 1           5           10           15

Ala Leu Ala Ala Pro Cys Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
      20           25           30
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
      35           40           45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
      50           55           60
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
      65           70           75           80
Ser Leu Glu Lys Arg Glu Ala Glu Ala
      85

```

&lt;210&gt; 30

&lt;211&gt; 2952

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 30

```

atgagatttc cttcaatttt tactgctggt ttattcgcag catcctccgc attagctgct      60
ccagtcaaca ctacaacaga agatgaaacg gcacaaattc cggctgaagc tgtcatcggt      120
tactcagatt tagaagggga ttctgatggt gctgttttgc cattttccaa cagcacaaat      180
aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta      240
tctctcgaga aaagagctgg cgctgatgat gtcgtcgact cctccaagtc cttcgatcatg      300
gagaacttcg cttcctacca cgggaccaag ccaggttacg tcgactccat ccagaagggt      360
atccagaagc caaagtccgg cacccaaggt aactacgacg acgactggaa ggggttctac      420
tccaccgaca acaagtacga cgctgcggga tactctgtag ataatgaaaa cccgctctct      480
ggaaaagctg gaggcgtggt caaagtgcag tatccaggac tgacgaaggt tctcgacta      540
aaagtggata atgccgaaac tattaagaaa gagttagggt taagtctcac tgaaccgttg      600
atggagcaag tcggaacgga agagtttatc aaaaggttcg gtgatgggtgc ttcgctgta      660
gtgctcagcc ttcccttcgc tgaggggagt tctagcgttg aatatattaa taactgggaa      720
caggcgaag cgtaagcgt agaacttgag attaattttg aaaccctggg aaaacgtggc      780
caagatgcga tgtatgagta tatggctcaa gcctgtgcag gaaatcgtgt caggcgatca      840
gtaggtgact cattgtcatg cataaatctt gattgggatg tcataaggga taaaactaag      900
acaaagatag agtctttgaa agagcatggc ccaatcaaga acaagatgtc cgaatcccc      960
gctaagaccg tctccgagga aaaggccaag caatacctag aagagttcca ccaaaccgcc      1020
ttggagcatc ctgaattgtc agaacttaaa accgttactg ggaccaatcc tgtattcgct      1080
ggggctaact atgcggcgtg ggcagtaaac gttgcgcaag ttatcgatag cgaacagct      1140
gataatttgg aaaagacaac tgctgtctct tcgatacttc ctgggtatcg tagcgtaatg      1200
ggcattgcag acggtgccgt tcaccacaat acagaagaga tagtggcaca atccatcgct      1260
ttgtcctctt tgatggttgc tcaagotatc ccattggtcg gtgagttggt tgacatcggt      1320
ttcgctgcct acaacttcgt cgagtcctac atcaacttgt tccaagtcgt ccacaactcc      1380
tacaaccgtc cggcttactc cccaggtcac aagaccaaac cattcttgcc atgggacatc      1440
cagatgacc agaccacctc ctccctgtct gctcctctgg gcgacagagt caccatcagt      1500
tgcagggcaa gtcaggacat tagaaattat ttaaactggt atcaacagaa accagatgga      1560
actgttaaac tcttgatcta ctacacatca agattacagt caggagtccc atcaaagtcc      1620
agtggcagtg ggtctggaac agattattct ctaccatta gcaacctgga gcaagaggat      1680
attgccactt acttttgcca acagggtaat acgcttccgt ggacgttcgc tggaggcacc      1740
aagctggaga taaaaggagg cggaggcagc ggaggcgttg gctcgggagg gggaggctcg      1800
gaggtgcagc tccagcagtc tggacctgag ctggtgaagc ctggagcttc aatgaagata      1860
tcttgaagg cttctgggta ctattcagc ggctacacca tgaactgggt gaagcagagt      1920
catggaaaga accttgagtg gatgggactt attaatcctt acaaaggtgt tagtacctac      1980
aaccagaagt tcaaggacaa ggccacatta actgtagaca agtcatccag cacagcctac      2040
atggaactcc tcagtctgac atctgaggac tctgcagtct attactgtgc aagatcgggg      2100

```

25

```

tactacggtg atagtgactg gtacttcgat gtctggggcg caggcaccac tgtcacagtc 2160
tcctcaggag gtggcggatc cggaggaggc ggtagtggcg gaggcggttc ggacatccag 2220
atgaccaga ccacctctc cctgtctgcc tccctggcg acagagtcac catcagttgc 2280
agggcaagtc aggacattag aaattattta aactgggtatc aacagaaacc agatggaact 2340
gttaaactcc tgatctacta cacatcaaga ttacactcag gaggcccatc aaagttcagt 2400
ggcagtggtg ctggaacaga ttattctctc accattagca acctggagca agaggatatt 2460
gccacttact tttgccaca gggtaatacg cttccgtgga cgttcgctgg aggcaccaag 2520
ctggagataa aaggaggcgg aggcagcgga ggcggtggct cgggaggggg aggctcggag 2580
gtgcagctcc agcagtctgg acctgagctg gtgaagcctg gagcttcaat gaagatatcc 2640
tgcaaggctt ctggttactc attcactggc tacaccatga actgggtgaa gcagagtcac 2700
ggaaagaacc ttgagtggat gggacttatt aatccttaca aaggtgttag tacctacaac 2760
cagaagttca aggacaaggc cacattaact gtagacaagt catccagcac agcctacatg 2820
gaactcctca gtctgacatc tgaggactct gcagtctatt actgtgcaag atcgggggtac 2880
tacggtgata gtgactggta cttcgatgtc tggggccaag gcaccactct cacagttctc 2940
tcatgagaat tc 2952

```

&lt;210&gt; 31

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 31

```

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1           5           10           15
Ala Leu Ala Ala Pro Cys Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20           25           30
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35           40           45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50           55           60
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65           70           75           80
Ser Leu Glu Lys Arg
85

```

&lt;210&gt; 32

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;400&gt; 32

```

Ala Ile His Arg Gly Gly Gly
1           5

```

&lt;210&gt; 33

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 33

```

gccatccacc gaggaggtgg t

```

21

26

<210> 34  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 34  
 Met Gly Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ala Asp Ala Ala  
 20

<210> 35  
 <211> 210  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 35  
 gttcaccaca atacagaaga gatagtggca caatccatcg ctttgtcctc tttgatggtt 60  
 gctcaagcta tccattggt cggtgagttg gttgacatcg gtttcgctgc ctacaacttc 120  
 gtcgagtcca tcatcaactt gttccaagtc gtccacaact cctacaaccg tccggcttac 180  
 tccccagggtc acaagacca accattcttg 210

<210> 36  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 36  
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met  
 20

<210> 37  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <400> 37  
 Ala Ser Ala Gly Gly Ser  
 1 5

<210> 38  
 <211> 642  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 38

Gly	Ala	Asp	Asp	Val	Val	Asp	Ser	Ser	Lys	Ser	Phe	Val	Met	Glu	Asn
1				5					10					15	
Phe	Ser	Ser	Tyr	His	Gly	Thr	Lys	Pro	Gly	Tyr	Val	Asp	Ser	Ile	Gln
			20					25					30		
Lys	Gly	Ile	Gln	Lys	Pro	Lys	Ser	Gly	Thr	Gln	Gly	Asn	Tyr	Asp	Asp
		35					40					45			
Asp	Trp	Lys	Gly	Phe	Tyr	Ser	Thr	Asp	Asn	Lys	Tyr	Asp	Ala	Ala	Gly
	50					55					60				
Tyr	Ser	Val	Asp	Asn	Glu	Asn	Pro	Leu	Ser	Gly	Lys	Ala	Gly	Gly	Val
65					70					75					80
Val	Lys	Val	Thr	Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu	Ala	Leu	Lys	Val
				85					90					95	
Asp	Asn	Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu	Ser	Leu	Thr	Glu
			100					105					110		
Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile	Lys	Arg	Phe	Gly
		115					120					125			
Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe	Ala	Glu	Gly	Ser
	130					135					140				
Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu	Gln	Ala	Lys	Ala	Leu	Ser
145					150					155					160
Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu	Thr	Arg	Gly	Lys	Arg	Gly	Gln	Asp
				165					170					175	
Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly	Asn	Arg	Val	Arg
			180					185					190		
Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp	Trp	Asp	Val
		195					200					205			
Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys	Glu	His	Gly
	210					215					220				
Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Asn	Lys	Thr	Val	Ser	Glu
225					230					235					240
Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln	Thr	Ala	Leu	Glu
				245					250					255	
His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly	Thr	Asn	Pro	Val
			260					265					270		
Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn	Val	Ala	Gln	Val
		275					280					285			
Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Thr	Ala	Ala	Leu
	290					295					300				
Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala	Asp	Gly	Ala
305					310					315					320
Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile	Ala	Leu	Ser
				325					330					335	
Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu	Leu	Val	Asp
			340					345					350		
Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile	Ile	Asn	Leu	Phe
		355					360					365			
Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr	Ser	Pro	Gly	His
	370					375					380				
Lys	Thr	Gln	Pro	Phe	Ala	Ser	Ala	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr
385					390					395					400
Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile
				405					410					415	
Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln
			420					425					430		
Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg
		435					440					445			



28

```

Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr
  450          455          460
Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr
  465          470          475          480
Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly
          485          490          495
Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Gly Ser Gly Gly Gly Ser
          500          505          510
Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly
          515          520          525
Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala
          530          535          540
Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser
  545          550          555          560
His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly
          565          570          575
Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val
          580          585          590
Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser
          595          600          605
Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp
  610          615          620
Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val
  625          630          635          640
Ser Ser

```

<210> 39  
 <211> 656  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct

```

<400> 39
Gly Ser Ser His His His His His Ser Ser Ser Gly Leu Val Pro Arg
  1          5          10          15
Gly Ser His Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val
          20          25          30
Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp
          35          40          45
Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn
          50          55          60
Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp
  65          70          75          80
Ala Ala Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala
          85          90          95
Gly Gly Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala
          100          105          110
Leu Lys Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser
          115          120          125
Leu Thr Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys
          130          135          140
Arg Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala
  145          150          155          160
Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys
          165          170          175
Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg
          180          185          190

```

Gly	Gln	Asp	Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly	Asn
		195					200					205			
Arg	Val	Arg	Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp
	210					215					220				
Trp	Asp	Val	Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys
225					230					235					240
Glu	His	Gly	Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Asn	Lys	Thr
				245					250					255	
Val	Ser	Glu	Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln	Thr
			260					265					270		
Ala	Leu	Glu	His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly	Thr
		275					280					285			
Asn	Pro	Val	Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn	Val
	290					295					300				
Ala	Gln	Val	Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Thr
305					310					315					320
Ala	Ala	Leu	Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala
				325					330					335	
Asp	Gly	Ala	Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile
			340					345					350		
Ala	Leu	Ser	Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu
		355					360					365			
Leu	Val	Asp	Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile	Ile
	370					375					380				
Asn	Leu	Phe	Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr	Ser
385					390					395					400
Pro	Gly	His	Lys	Thr	Gln	Pro	Phe	Leu	Pro	Trp	Asp	Ile	Gln	Met	Thr
				405					410					415	
Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile
			420					425					430		
Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln
		435					440					445			
Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg
	450					455					460				
Leu	His	Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
465					470					475					480
Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr
				485					490					495	
Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly	Gly
			500					505					510		
Thr	Lys	Leu	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		515					520					525			
Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu
	530					535					540				
Leu	Val	Lys	Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly
545					550					555					560
Tyr	Ser	Phe	Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly
				565					570					575	
Lys	Asn	Leu	Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val	Ser
				580				585					590		
Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Phe	Thr	Val	Asp	Lys
		595					600					605			
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr	Ser	Glu	Asp
	610					615					620				
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Gly	Tyr	Tyr	Gly	Asp	Ser	Asp
625					630					635					640
Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Phe	Ser
				645					650					655	

<210> 40  
 <211> 1943  
 <212> DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 40

ccatggggcgc	tgatgatggt	gttgattctt	ctaaatcttt	tgtgatggaa	aacttttctt	60
cgtaccacgg	gactaaacct	ggttatgtag	attccattca	aaaaggtata	caaaagccaa	120
aatctggtac	acaaggaaat	tatgacgatg	attggaaagg	gttttatagt	accgacaata	180
aatacgacgc	tgcgggatac	tctgtagata	atgaaaaccc	gctctctgga	aaagctggag	240
gcgtgggtcaa	agtgaagtat	ccaggactga	cgaagggtct	cgactaaaaa	gtggataatg	300
ccgaaactat	taagaaagag	ttaggtttaa	gtctcactga	accgttgatg	gagcaagtcg	360
gaacggaaga	gtttatcaaa	aggttcggtg	atgggtgctc	gcgtgtagtg	ctcagccttc	420
ccttcgctga	ggggagttct	agcgttgaat	atattaataa	ctgggaacag	gcgaaagcgt	480
taagcgtaga	acttgagatt	aattttgaaa	cccgtggaaa	acgtggccaa	gatgcatgtg	540
atagatatat	ggctcaagcc	tgtgcaggaa	atcgtgtcag	gcgatcagta	ggtagctcat	600
tgtcatgcat	aaatcttgat	tgggatgtca	taagggataa	aactaagaca	aagatagagt	660
ctttgaaaga	gcatggccct	atcaaaaaata	aatgagcgga	aagtcccaat	aaaacagtat	720
ctgaggaaaa	agctaaacaa	tacctagaag	aatttcatca	aacggcatta	gagcatcctg	780
aattgtcaga	acttaaaacc	gttactggga	ccaatcctgt	attcgctggg	gctaactatg	840
cggcgtgggc	agtaaacggt	gcgcaagtta	tcgatagcga	aacagctgat	aattttgaaa	900
agacaactgc	tgctctttcg	atacttcctg	gtatcggtag	cgtaatgggc	attgcagacg	960
gtgccgttca	ccacaatata	gaagagatag	tggcacaatc	aatagcttta	tcgtctttaa	1020
tggttgctca	agctattcca	ttggtaggag	agctagttga	tattggtttc	gctgcatata	1080
attttgtaga	gagtattatc	aatttatattc	aagtagttca	taattcgtat	aatcgtcccg	1140
cgtattctcc	ggggcataaa	acgcaaccat	ttgcttcctc	cggtaggatcc	gacatccaga	1200
tgaccagac	cacctcctcc	ctgtctgcct	ctctgggaga	cagagtcacc	atcagttgca	1260
gggcaagtc	ggacattaga	aattatttaa	actgggtatca	acagaaacca	gatggaactg	1320
ttaaactcct	gactactac	acatcaagat	tacactcagg	agtcccatca	aagttcagtg	1380
gcagtgggtc	tggaacagat	tattctctca	ccattagcaa	cctggagcaa	gaggatattg	1440
ccacttactt	ttgccaacag	ggtaatacgc	ttccgtggac	gttcgctgga	ggcaccaagc	1500
tggaaatcaa	acgggctgga	ggcggtagtg	gcggtggatc	aggtggaggc	agcgggtggc	1560
gatctgaggt	gcagctccag	cagtctggac	ctgagctggt	gaagcctgga	gcttcaatga	1620
agatatcctg	caaggcttct	ggttactcat	tcactggcta	caccatgaac	tgggtgaagc	1680
agagtcatgg	aaagaacctt	gagtggatgg	gacttattaa	tccttacaaa	ggtgttagta	1740
cctacaacca	gaagttcaag	gacaaggcca	cattaactgt	agacaagtca	tccagcacag	1800
cctacatgga	actcctcagt	ctgacatctg	aggactctgc	agtctattac	tgtgcaagat	1860
cgggggtacta	cggtgatagt	gactggtaact	tcgatgtctg	gggcgcaggg	accacgggtca	1920
ccgtctcctc	atgatagaga	tct				1943

&lt;210&gt; 41

&lt;211&gt; 1940

&lt;212&gt; DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 41

tgggcgctga	tgatgttggt	gattcttcta	aatcttttgt	gatggaaaac	ttttcttcgt	60
accacgggac	taaacctggg	tatgtagatt	ccattcaaaa	aggtatacaa	aagccaaaat	120
ctggtacaca	aggaaattat	gacgatgatt	ggaaaagggt	ttatagtacc	gacaataaat	180
acgacgctgc	gggatactct	gtagataatg	aaaacccgct	ctctggaaaa	gctggaggcg	240
tggtcaaagt	gacgtatcca	ggactgacga	aggttctcgc	actaaaagtg	gataatgccg	300
aaactattaa	gaaagagtta	ggtttaagtc	tcactgaacc	gttgatggag	caagtcggaa	360
cgggaagagt	tatcaaaaagg	ttcgggtgatg	gtgcttcgcg	tgtagtgtct	agccttccct	420
tcgctgaggg	gagttctagc	gttgaatata	ttaataaact	ggaacaggcg	aaagcggtta	480
gcgtagaact	tgagattaat	tttgaaaccc	gtggaaaacg	tggccaagat	gcgatgtatg	540
agtatatggc	tcaagcctgt	gcaggaaatc	gtgtcaggcg	atcagtaggt	agctcattgt	600
catgcataaa	tcttgattgg	gatgtcataa	gggataaaac	taagacaaag	atagagtctt	660

```

tgaaagagca tggccctatc aaaaataaaa tgagcgaaag tcccaataaa acagtatctg      720
aggaaaaagc taaacaatac ctagaagaat ttcatacaaac ggcattagag catcctgaat      780
tgtcagaact taaaaccgtt actgggacca atcctgtatt cgctggggct aactatgcgg      840
cgtgggcagt aaacgttgcg caagttatcg atagcgaaac agctgataat ttggaaaaga      900
caactgctgc tctttcgata cttcctggta tcggtagcgt aatgggcatt gcagacggtg      960
ccgttcacca caatacagaa gagatagtgg cacaatcaat agctttatcg tctttaatgg     1020
ttgctcaagc tattccattg gtaggagagc tagttgatat tggtttcgct gcatataatt     1080
ttgtagagag tattatcaat ttatttcaag tagttcataa ttcgtataat cgtcccgctg     1140
attctccggg gcataaaacg caaccatttg ctcccgccgg tggatccgac atccagatga     1200
cccagaccac ctccctccctg tctgcctctc tgggagacag agtcaccatc agttgcaggg     1260
caagtcagga cattagaaat tattttaaact ggtatcaaca gaaaccagat ggaactgtta     1320
aactcctgat ctactacaca tcaagattac actcaggagt cccatcaaag ttcagtggca     1380
gtgggtctgg aacagattat tctctcacca ttagcaacct ggagcaagag gatattgcca     1440
cttacttttg ccaacagggg aatacgcctt cgtggacgtt cgctggaggc accaagctgg     1500
aaatcaaacg ggctggaggc ggtagtggcg gtggatcagg tggaggcagc ggtggcggat     1560
ctgaggtgca gctccagcag tctggacctg agctggtgaa gcctggagct tcaatgaaga     1620
tattcctgaa ggcttctggt tactcattca ctggctacac catgaactgg gtgaagcaga     1680
gtcatggaaa gaaccttgag tggatgggac ttattaatcc ttacaaaggt gttagtacct     1740
acaaccagaa gttcaaggac aaggccacat taactgtaga caagtcatcc agcacagcct     1800
acatggaact cctcagtcct acatctgagg actctgcagt ctattactgt gcaagatcgg     1860
ggtactacgg tgatagtgcg tgggtacttc atgtctgggg cgcagggacc acggtcaccg     1920
tctcctcatg atagagatct                                     1940

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<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 42

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Pro Gly Gly Asn Arg Gly Thr Thr Arg Pro Ala Thr Ser Gly Ser Ser
 1             5             10             15
Pro Gly Pro Thr Asn Ser His Tyr
                20

```

<210> 43

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 43

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1             5             10             15

```

<210> 44

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 44

cgggatccag tcgacatgga gacagacaca ctctgttat gggactgct gctctgggtt 60  
cca 63

<210> 45  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 45  
gtactgctgc tctgggttcc aggtgccgac gctgctggcg ctgatgatgt tgttgat 57

<210> 46  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 46  
atagaattct tagtggtggt ggtggtggtg tgagaagact gtgagagtgg tgcctt 56

<210> 47  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 47  
Glu Ala Glu Ala Tyr Val Glu Phe  
1 5

<210> 48  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 48  
Glu Ala Tyr Val Glu Phe  
1 5

<210> 49  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 49  
 Tyr Val Glu Phe  
 1

<210> 50  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 50  
 tataacatgg gcgctgatga tggtgttgat 30

<210> 51  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 51  
 actgccacg ccgcatagtt agc 23

<210> 52  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 52  
 ttgcgcaacg tttactgccc acgccgcata gttagccc 38

<210> 53  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 53  
 cgctatcgat aacttgcgca acgtttactg ccc 33

<210> 54  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 54  
 gcagttgtct tttccaaatt atcagctggt tcgctatcga taac 44

<210> 55  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 55  
gctaccgata ccaggaagta tcgaaagagc agcagttgtc ttttcc 46

<210> 56  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 56  
gaacggcacc gtctgcaatg cccattacgc taccgatacc aggaagtatc gaaagag 57

<210> 57  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 57  
actatctctt ctgtattgtg gtgaacggca ccgtctgcaa tg 42

<210> 58  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 58  
caaccattaa agacgataaa gctattgatt gtgcactat ctcttctg 48

<210> 59  
<211> 80  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 59  
ctacaaaatt atatgcagcg aaaccaatat caactagctc tcctaccaat ggaatagctt 60  
gagcaaccat taaagacgat 80

<210> 60

<211> 66  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct  
  
 <400> 60  
 cgattatacg aattatgaac tacttgaaat aaattgataa tactctctac aaaattatat 60  
 gcagcg 66  
  
 <210> 61  
 <211> 83  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct  
  
 <400> 61  
 gcgaattcgg atccaccggc ggaagcaaat ggttgcggtt tatgccccgg agaatacgcg 60  
 ggacgattat acgaattatg aac 83  
  
 <210> 62  
 <211> 83  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct  
  
 <400> 62  
 gcgaattcgg atccaccggc ggaagcaaat ggttgcggtt tatgccccgg agaatacgcg 60  
 ggacgattat acgaattatg aac 83  
  
 <210> 63  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct  
  
 <400> 63  
 aagtagttca taattcgtat aatcgtcccg cgtattctcc g 41  
  
 <210> 64  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:/Note =  
       synthetic construct  
  
 <400> 64  
 gcggatccga catccagatg acccagacca cc 32



36

<210> 65  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 65

cctctagaag cccgtttgat ttccagcttg gt

32

<210> 66  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 66

ccgtcgacga ggtgcagctc cagcagtct

29

<210> 67  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 67

ccaagctttc atgaggagac ggtgaccgtg gtccc

35

<210> 68  
 <211> 657  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 68

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5				10					15		
Arg	Gly	Ser	His	Gly	Ala	Asp	Asp	Val	Val	Asp	Ser	Ser	Lys	Ser	Phe
			20					25					30		
Val	Met	Glu	Asn	Phe	Ser	Ser	Tyr	His	Gly	Thr	Lys	Pro	Gly	Tyr	Val
		35					40					45			
Asp	Ser	Ile	Gln	Lys	Gly	Ile	Gln	Lys	Pro	Lys	Ser	Gly	Thr	Gln	Gly
		50				55					60				
Asn	Tyr	Asp	Asp	Asp	Trp	Lys	Gly	Phe	Tyr	Ser	Thr	Asp	Asn	Lys	Tyr
65					70				75					80	
Asp	Ala	Ala	Gly	Tyr	Ser	Val	Asp	Asn	Glu	Asn	Pro	Leu	Ser	Gly	Lys
			85						90					95	
Ala	Gly	Gly	Val	Val	Lys	Val	Thr	Tyr	Pro	Gly	Leu	Thr	Lys	Val	Leu
			100					105						110	

Ala	Leu	Lys	Val	Asp	Asn	Ala	Glu	Thr	Ile	Lys	Lys	Glu	Leu	Gly	Leu
	115						120					125			
Ser	Leu	Thr	Glu	Pro	Leu	Met	Glu	Gln	Val	Gly	Thr	Glu	Glu	Phe	Ile
	130					135					140				
Lys	Arg	Phe	Gly	Asp	Gly	Ala	Ser	Arg	Val	Val	Leu	Ser	Leu	Pro	Phe
145					150					155					160
Ala	Glu	Gly	Ser	Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu	Gln	Ala
				165					170					175	
Lys	Ala	Leu	Ser	Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu	Thr	Arg	Gly	Lys
			180					185					190		
Arg	Gly	Gln	Asp	Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly
		195					200					205			
Asn	Arg	Val	Arg	Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu
	210					215					220				
Asp	Trp	Asp	Val	Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu
225					230					235					240
Lys	Glu	His	Gly	Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Asn	Lys
				245					250					255	
Thr	Val	Ser	Glu	Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln
			260					265					270		
Thr	Ala	Leu	Glu	His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly
		275					280					285			
Thr	Asn	Pro	Val	Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn
	290					295					300				
Val	Ala	Gln	Val	Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr
305					310					315					320
Thr	Ala	Ala	Leu	Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile
				325					330					335	
Ala	Asp	Gly	Ala	Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser
			340					345					350		
Ile	Ala	Leu	Ser	Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly
		355					360					365			
Glu	Leu	Val	Asp	Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile
	370					375					380				
Ile	Asn	Leu	Phe	Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr
385					390					395					400
Ser	Pro	Gly	His	Lys	Thr	Gln	Pro	Phe	Leu	Pro	Trp	Asp	Ile	Gln	Met
				405					410					415	
Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr
			420					425					430		
Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr
		435					440					445			
Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser
		450				455					460				
Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly
465					470					475					480
Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala
				485					490					495	
Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly
			500					505					510		
Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
		515					520					525			
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro
		530				535					540				
Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser
545					550					555					560
Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His
				565					570					575	
Gly	Lys	Asn	Leu	Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val
			580					585					590		
Ser	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Phe	Thr	Val	Asp
		595					600						605		

Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu  
 610 615 620  
 Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser  
 625 630 635 640  
 Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe  
 645 650 655  
 Ser

<210> 69

<211> 643

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 69

Met Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu  
 1 5 10 15  
 Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile  
 20 25 30  
 Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp  
 35 40 45  
 Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala  
 50 55 60  
 Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly  
 65 70 75 80  
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys  
 85 90 95  
 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr  
 100 105 110  
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe  
 115 120 125  
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly  
 130 135 140  
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu  
 145 150 155 160  
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln  
 165 170 175  
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val  
 180 185 190  
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp  
 195 200 205  
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His  
 210 215 220  
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser  
 225 230 235 240  
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu  
 245 250 255  
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro  
 260 265 270  
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln  
 275 280 285  
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala  
 290 295 300

Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly  
 305 310 315 320  
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu  
 325 330 335  
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val  
 340 345 350  
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu  
 355 360 365  
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly  
 370 375 380  
 His Lys Thr Gln Pro Phe Ala Ser Ala Gly Gly Ser Asp Ile Gln Met  
 385 390 395 400  
 Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr  
 405 410 415  
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr  
 420 425 430  
 Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Thr Ser  
 435 440 445  
 Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly  
 450 455 460  
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala  
 465 470 475 480  
 Thr Tyr Phe Cys Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly  
 485 490 495  
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Gly Gly Gly Ser Gly Gly Gly  
 500 505 510  
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser  
 515 520 525  
 Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys  
 530 535 540  
 Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln  
 545 550 555 560  
 Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys  
 565 570 575  
 Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr  
 580 585 590  
 Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr  
 595 600 605  
 Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly  
 610 615 620  
 Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr  
 625 630 635 640  
 Val Ser Ser

&lt;210&gt; 70

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

&lt;400&gt; 70

 Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu  
 1 5 10

<210> 71  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 71  
atgagcgaag gtcccaataa aacagtatct gaggaag 36

<210> 72  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 72  
gagcgaaagt cccagaaga cagtatctga gg 32

<210> 73  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 73  
gaagacgaag ac 12

<210> 74  
<211> 36  
<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 74  
gtcttcgtct tcgtcttcgt cttcgtcttc gtcttc 36

<210> 75  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 75  
Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu  
1 5 10

<210> 76  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 76  
atgagcgaataa gtccaataa aacagtatct gaggaa 36

<210> 77  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 77  
gagcgaaagt ccggccaaaa cagtatctga gg 32

<210> 78  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 78  
cggcca 6

<210> 79  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 79  
tggccg 6

<210> 80  
<211> 14  
<212> PRT  
<213> Artificial Sequence

42

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 80

Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu Glu Lys Ala  
1 5 10

&lt;210&gt; 81

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 81

atgagcgaataa gtcccaataa aacagtatct gaggaataaac ct

42

&lt;210&gt; 82

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 82

gagcgaaagt cccaataaag cgggtctctga ggaaaaacc

39

&lt;210&gt; 83

&lt;211&gt; 6

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 83

ggtctc

6

&lt;210&gt; 84

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
synthetic construct

&lt;400&gt; 84

gagaccgaga ccgagaccga gaccgagacc

30

&lt;210&gt; 85

&lt;211&gt; 12

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 85  
Ser Phe Val Met Glu Asn Phe Ser Ser Tyr His Gly  
1 5 10

<210> 86  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 86  
tcttttgtga tggaaaactt ttcttcgtac cacggg 36

<210> 87  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 87  
cttttgtgat ggaagctttt tcttcgtacc acg 33

<210> 88  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 88  
aagctt 6

<210> 89  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 89  
aagctt 6



44

<210> 90  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 90  
Phe Val Met Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro  
1 5 10

<210> 91  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 91  
tttgtgatgg aaaacttttc ttcgtaccac gggactaaac ct

42

<210> 92  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 92  
gtgatggaaa actttgctag ctaccacggg actaaacc

38

<210> 93  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 93  
gctagc

6

<210> 94  
<211> 6  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 94  
gctagc 6

<210> 95  
<211> 180  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 95  
ggcgctgatg atgttggtga ttcttctaaa tcttttgtga tggaaaactt ttcttcgtac 60  
cacgggacta aacctgggta tgtagattcc attcaaaaag gtatacaaaa gccaaaatct 120  
ggtacacaag gaaattatga cgatgattgg aaaggggttt atagtaccga caataaatac 180

<210> 96  
<211> 180  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 96  
ggcgctgatg atgtcgtcga ctctccaag tccttcgtca tggagaactt cgcttcctac 60  
cacgggacca agccagggta cgtcgactcc atccagaagg gtatccagaa gccaaagtcc 120  
ggcacccaag gtaactacga cgacgactgg aaggggttct actccaccga caacaagtac 180

<210> 97  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 97  
aaagagcatg gccctatcaa aaataaaatg agcgaaagtc ccaataaaac agtatctgag 60  
gaaaaagcta aacaatacct agaagaattt catcaaacgg cattagagca tcctgaattg 120

<210> 98  
<211> 120  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/Note =  
synthetic construct

<400> 98  
aaagagcatg gcccaatcaa gaacaagatg tccgaatccc ccgctaagac cgtctccgag 60  
gaaaaggcca agcaatacct agaagagttc caccaaaccg ccttgagca tcctgaattg 120

<210> 99  
 <211> 210  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 synthetic construct

<400> 99  
 gttcaccaca atacagaaga gatagtggca caatcaatag ctttatcgtc tttaatggtt 60  
 gctcaagcta ttccattggg aggagagcta gttgatattg gtttcgctgc atataatttt 120  
 gtagagagta ttatcaattt atttcaagta gttcataatt cgtataatcg tcccgcgat 180  
 tctccggggc ataaaacgca accatttctt 210

<210> 100  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 100  
 ccctgcacgc cgatgctatc cacagaagag gaggacaagt cattccaacc atgaag 56

<210> 101  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 101  
 gccgatgcta tccacagaag a 21

<210> 102  
 <211> 2691  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 102  
 gctgggtgctg acgacgtcgt cgactcctcc aagtccttcg tcatggagaa cttcgcttcc 60  
 taccacggga ccaagccagg ttacgtcgac tccatccaga agggatatcca gaagccaaag 120  
 tccggcacc caggtaacta cgacgacgac tggaaggggt tctactccac cgacaacaag 180  
 tacgacgctg cgggatactc tgtagataat gaaaaccgc tctctggaaa agctggaggc 240  
 gtggtcaagg tcacctacc aggtctgact aaggtcttgg ctttgaagg cgaacaacgct 300  
 gagaccatca agaaggagt gggtttgtcc ttgactgagc cattgatgga gcaagtcggg 360  
 accgaagagt tcatcaagag attcgggtgac ggtgcttcca gagtcgtctt gtccttgcca 420  
 ttcgctgagg gttcttctag cgttgaatat attaataact gggaacaggc taaggccttg 480

tctgttgaat	tggagattaa	cttcgaaacc	agaggtaaga	gaggtcaaga	tgcgatgtat	540
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&lt;210&gt; 103

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 103

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr

1

5

10

15

Asp Ala Arg Cys

20

&lt;210&gt; 104

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 104  
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10 15

<210> 105  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 105  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 106  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 106  
Met Leu Ala Asp Asp  
1 5

<210> 107  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 107  
Met Leu Asp Asp  
1

<210> 108  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 108  
Ser Ala Asp Asp

1

&lt;210&gt; 109

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 109

Ser Pro Gly Ala Asp Asp

1

5

&lt;210&gt; 110

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 110

Gly Ala Asp Asp

1

&lt;210&gt; 111

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 111

Met Gly Ala Asp Asp

1

5

&lt;210&gt; 112

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 112

Met Ala Ala Asp Asp

1

5

&lt;210&gt; 113

&lt;211&gt; 4

&lt;212&gt; PRT

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 113  
Ala Ala Asp Asp  
1

<210> 114  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 114  
Met Ser Ala Asp Asp  
1 5

<210> 115  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 115  
Met Gly Ser Asp Asp  
1 5

<210> 116  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 116  
Met Gly Gly Asp Asp  
1 5

<210> 117  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

51

<400> 117  
Met Gly Val Asp Asp  
1 5

<210> 118  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 118  
Gly Gly Asp Asp  
1

<210> 119  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 119  
Gly Val Asp Asp  
1

<210> 120  
<211> 652  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 120  
Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu  
1 5 10 15  
Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile  
20 25 30  
Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp  
35 40 45  
Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala  
50 55 60  
Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly  
65 70 75 80  
Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys  
85 90 95  
Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr  
100 105 110  
Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe  
115 120 125  
Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly  
130 135 140



Ser	Ser	Ser	Val	Glu	Tyr	Ile	Asn	Asn	Trp	Glu	Gln	Ala	Lys	Ala	Leu
145					150					155					160
Ser	Val	Glu	Leu	Glu	Ile	Asn	Phe	Glu	Thr	Arg	Gly	Lys	Arg	Gly	Gln
				165					170						175
Asp	Ala	Met	Tyr	Glu	Tyr	Met	Ala	Gln	Ala	Cys	Ala	Gly	Asn	Arg	Val
			180					185					190		
Arg	Arg	Ser	Val	Gly	Ser	Ser	Leu	Ser	Cys	Ile	Asn	Leu	Asp	Trp	Asp
		195					200					205			
Val	Ile	Arg	Asp	Lys	Thr	Lys	Thr	Lys	Ile	Glu	Ser	Leu	Lys	Glu	His
	210					215					220				
Gly	Pro	Ile	Lys	Asn	Lys	Met	Ser	Glu	Ser	Pro	Ala	Lys	Thr	Val	Ser
225					230					235					240
Glu	Glu	Lys	Ala	Lys	Gln	Tyr	Leu	Glu	Glu	Phe	His	Gln	Thr	Ala	Leu
				245					250						255
Glu	His	Pro	Glu	Leu	Ser	Glu	Leu	Lys	Thr	Val	Thr	Gly	Thr	Asn	Pro
			260					265					270		
Val	Phe	Ala	Gly	Ala	Asn	Tyr	Ala	Ala	Trp	Ala	Val	Asn	Val	Ala	Gln
	275						280					285			
Val	Ile	Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Thr	Ala	Ala
	290					295					300				
Leu	Ser	Ile	Leu	Pro	Gly	Ile	Gly	Ser	Val	Met	Gly	Ile	Ala	Asp	Gly
305					310					315					320
Ala	Val	His	His	Asn	Thr	Glu	Glu	Ile	Val	Ala	Gln	Ser	Ile	Ala	Leu
				325					330						335
Ser	Ser	Leu	Met	Val	Ala	Gln	Ala	Ile	Pro	Leu	Val	Gly	Glu	Leu	Val
			340					345					350		
Asp	Ile	Gly	Phe	Ala	Ala	Tyr	Asn	Phe	Val	Glu	Ser	Ile	Ile	Asn	Leu
	355						360					365			
Phe	Gln	Val	Val	His	Asn	Ser	Tyr	Asn	Arg	Pro	Ala	Tyr	Ser	Pro	Gly
	370					375					380				
His	Lys	Thr	Gln	Pro	Phe	Leu	Pro	Trp	Asp	Ile	Gln	Met	Thr	Gln	Thr
385					390					395					400
Thr	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys
				405					410						415
Arg	Ala	Ser	Gln	Asp	Ile	Arg	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys
			420					425					430		
Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His
		435					440					445			
Ser	Gly	Val	Pro	Ser	Lys	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr
	450					455					460				
Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe
465					470					475					480
Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Trp	Thr	Phe	Ala	Gly	Gly	Thr	Lys
				485					490						495
Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			500					505					510		
Gly	Gly	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys
		515					520					525			
Pro	Gly	Ala	Ser	Met	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe
	530					535					540				
Thr	Gly	Tyr	Thr	Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Asn	Leu
545					550					555					560
Glu	Trp	Met	Gly	Leu	Ile	Asn	Pro	Tyr	Lys	Gly	Val	Ser	Thr	Tyr	Asn
				565					570					575	
Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Phe	Thr	Val	Asp	Lys	Ser	Ser	Ser
			580					585					590		
Thr	Ala	Tyr	Met	Glu	Leu	Leu	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
		595					600					605			

53

Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe  
     610                    615                    620  
 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
 625                    630                    635                    640  
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
                     645                    650

&lt;210&gt; 121

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 121

Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser  
     1                    5                    10

&lt;210&gt; 122

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 122

Gly Ser Asp Asp  
     1